



SEQUENCE LISTING

<110> Maines, Mahin D.

<120> METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
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<170> PatentIn Ver. 2.1

<210> 1

<211> 296

<212> PRT

<213> Homo sapiens

<400> 1

Met Asn Ala Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
1 5 10 15

Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
20 25 30

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
35 40 45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
 130 135 140
 Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp
 145 150 155 160
 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
 165 170 175
 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
 180 185 190
 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
 195 200 205
 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
 210 215 220
 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
 225 230 235 240
 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
 245 250 255
 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
 260 265 270
 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
 275 280 285
 Gln Lys Tyr Cys Cys Ser Arg Lys
 290 295

<210> 2

<211> 1070

<212> DNA

<213> Homo sapiens

<400> 2

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 gatgctcttt ccagccaaga ggtggaggtc gcctatatct gcagtgagag ctccagccat 300
 gaggactaca tcaggcagtt ccttaatgct ggcaagcacg tccttgtgga ataccccatg 360
 acactgtcat tggcggccgc tcaggaactg tgggagctgg ctgagcagaa aggaaaagtc 420

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<210> 3

<211> 296

<212> PRT

<213> Homo sapiens

<400> 3

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Met Asn Thr Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
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Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
              20              25              30

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```

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
              35              40              45

```

```

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
  50              55              60

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```

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
  65              70              75              80

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```

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
              85              90              95

```

```

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
              100              105              110

```

```

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
              115              120              125

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Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
              130              135              140

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```

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
  145              150              155              160

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Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
210 215 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
225 230 235 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
260 265 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
275 280 285

Gln Lys Tyr Cys Cys Ser Arg Lys
290 295

<210> 4

<211> 295

<212> PRT

<213> Rattus norvegicus

<400> 4

Met Asp Ala Glu Pro Lys Arg Lys Phe Gly Val Val Val Val Gly Val
1 5 10 15

Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
20 25 30

Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
35 40 45

Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
50 55 60

Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu

65		70		75		80
Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu						
	85			90		95
Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu						
	100		105			110
Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu						
	115		120			125
Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu						
	130		135			140
Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg						
145		150		155		160
Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val						
	165		170			175
Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg						
	180		185			190
Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn						
	195		200			205
Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg						
	210		215			220
Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val						
225		230		235		240
Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile						
	245		250			255
Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala						
	260		265			270
Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln						
	275		280			285
Lys Leu Cys His Gln Lys Lys						
	290		295			

<210> 5

<211> 1081

<212> DNA

<213> Rattus norvegicus

<400> 5

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a 1081
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<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: hydrophobic
domain of BVR

<220>

<221> PEPTIDE

<222> (2)

<223> where X is any aa

<400> 6

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Phe Xaa Val Val Val Val
  1                      5
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<210> 7

<211> 6

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleotide
binding domain of BVR

<220>
<221> PEPTIDE
<222> (2)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (4)..(5)
<223> where X is any aa

<400> 7
Gly Xaa Gly Xaa Xaa Gly
1 5

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oxidoreductase domain of BVR

<400> 8
Ala Gly Lys His Val Leu Val Glu
1 5

<210> 9
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: leucine
zipper of BVR

<220>
<221> PEPTIDE
<222> (2)..(7)
<223> where X is any aa

<220>

<221> PEPTIDE
<222> (9)..(14)
<223> where X is any aa

<220>
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<222> (16)..(21)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (23)..(28)
<223> where X is any aa

<400> 9
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1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu
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<210> 10
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: kinase motif
of BVR

<400> 10
Ser Arg Arg
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<210> 11
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: kinase motif
of BVR

<400> 11
Lys Gly Ser
1

<210> 12
 <211> 3
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: kinase motif
 of BVR

 <220>
 <221> PEPTIDE
 <222> (3)
 <223> where X is any aa

 <400> 12
 Phe Gly Xaa
 1

 <210> 13
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: nuclear
 localization signal of BVR

 <400> 13
 Gly Leu Lys Arg Asn Arg Tyr
 1 5

 <210> 14
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: methylation
 site of BVR

 <400> 14
 Pro Gly Leu Lys Arg
 1 5

<210> 15
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: zinc finger
 domain of BVR

 <220>
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 <222> (3)..(12)
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 <400> 15
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<210> 16
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: protein
 kinase C enhancing domain

 <220>
 <221> PEPTIDE
 <222> (5)
 <223> where X is any aa

 <400> 16
 Lys Lys Arg Ile Xaa His Cys
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<210> 17
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: protein
 kinase C inhibiting domain

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<222> (3)
<223> where X is any aa

<220>
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<222> (5)..(7)
<223> where X is any aa

<400> 17
Gln Lys Xaa Cys Xaa Xaa Xaa Lys
1 5